Performance Analysis of Deep Learning Models for Biomedical Image Segmentation

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Introduction

- **Image Segmentation** is the process of **partitioning an image into multiple segments** into much more easier analysis able form [1].
- Cancer refers to **abnormal growth of cells**, it can either be **benign** or **malignant**
- In our work, we considered **two types** of **cancer: a) Brain, b) Skin**.
- **Skin cancer rates** in **India** is **high**, when compared with other countries like Canada, USA and UK [3] and is caused by over exposure to **ultraviolet rays** or **some genetic effect[3]**.
- Some different types of **brain cancer: Gliomas** (**High Grade Glioma** and **Low Grade Glioma)**, **Meningiomas**, **Pituitary adenomas**, gets their name from the **type of cells** involved.

Problem **Statement**

- **Cancer** can be **cured easily**, if it is found at **earlier stages**.
- With the **help of image segmentation**, it will be easy in **finding tumor shape, volume from medical imaging** and plan the **radiation treatment** for it accordingly.
- Since, **manual annotation** of this tumor region in medical imaging is **high time consuming** and is prone to **human errors** because of tumor having different sizes, shapes, contrast and locations[1].
- Thus, requires an accurate and reliable **automated segmentation techniques for segmenting this tumor from the medical imaging**, that can be useful for both **clinical** and **research purposes[1]**.
- Since deep learning is promising in most of the areas in the recent years, thus motivated us to use this in such important bio-medical task.

Literature Review

1

A Conditional Adversarial Network for Semantic Segmentation of Brain Tumor [1]

- For brain tumor segmentation : Conditional GAN (cGAN)
- Dataset: Brats 2017 brain tumor dataset.
- They considered three subsections of tumors: whole, core and enhancing (in both LGG and HGG patients)
- Evaluation parameters: Dice score (similarity score)
- Achieved about 0.80, 0.54, 0.59 for whole, core and enhancing tumor respectively

2

Adversarial Learning with Multi-scale Loss for Skin Lesion segmentation [3]

- Skin lesion segmentation: Segmentor Adversarial Network (SegAN)
- Dataset: ISIC 2017 skin lesion dataset
- The skin cancer in ISIC is melanoma
- Dice score of 0.86.

3

Association of genomic subtypes of lower-grade gliomas with shape features automatically extracted by a deep learning algorithm[2]

- Brain tumor image segmentation : U-Net.
- Dataset: Preprocessed version of BraTs 2015
- Considered Only LGG, 110 Subjects, Whole Tumor
- Dice score of 0.82

4

Skin lesion segmentation with deep learning[4]

- For Skin Lesion Segmentation, they used two architecture: a) TernausNet, b) DeepLabV3+.
- Dataset: ISIC 2018 Skin Cancer
- The evaluation parameter used is Jaccard Index.
- Data Augmentation: Rotation, Translation, Flipping etc.
- Model 1: Jaccard Index - 0.821, Model 2: Jaccard Index – 0.876

5

Skin Lesion Segmentation with C-Unet[5]

- For Skin Lesion Segmentation, they used C-UNet
- Dataset – ISIC 2018 skin cancer .
- Data Augmentation: Histogram equalization (to enhance color contrast of the image)
- Evaluation parameter used is Dice Score and Jaccard Index.
- Jaccard Index: 0.775, Dice Score: 0.869

6

SegNet-Based Gland Segmentation from Colon Cancer Histology Images[6]

- SegNet-based segmentation method for accurate segmenting the gland structures in colon cancer histology images.
- Dataset: Gland Segmentation Challenge in MICCAI 2015
- Data augmentation : random crop
- Evaluation parameter used Dice score and achieved 0.8636

Open Questions

- Can the SegNet and U-Net segmentation architectures be applied for brain tumor and skin lesion segmentation?

Objectives

1. To do performance analysis of Segmentor Adversarial Network on both skin and brain cancer dataset
2. To Perform Image Segmentation task on both Skin and Brain cancer dataset with **U-Net, SegNet**
3. Compare the results achieved from **U-Net, SegNet and SegAN (Skin Lesion ISIC 2018)**

Methodology

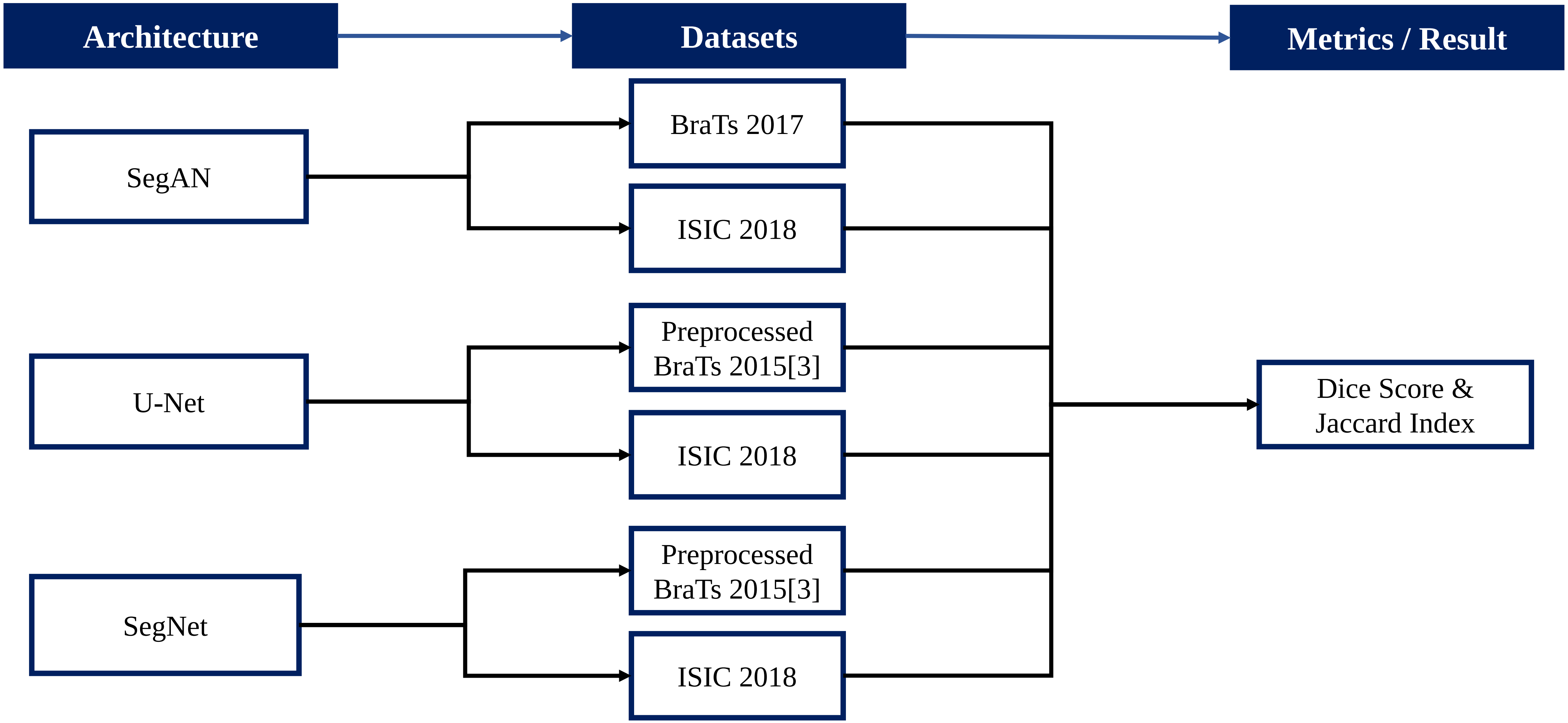


Figure 1: Flow chart of the project

Dataset Description

Dataset Description

1

BraTS 2017 Brain Tumor Dataset

- **135** Subjects **High-Grade Glioma** & **108** subjects of **Low-Grade Glioma** [8][9]
- Each subject, consist **4 MRI scans**: a) **T1-Weighted**, b) **T1-Gd, c) T2-Weighted** and d) **T2-FLAIR** and **two segmentation labels**: **manual** and **computer-aided**
- 3 **ground truth labels**: a) **Whole Tumor**, b) **Core Tumor**, c) **Enhancing Tumor**
- Each scan is **3D brain volume** (240x240x155)

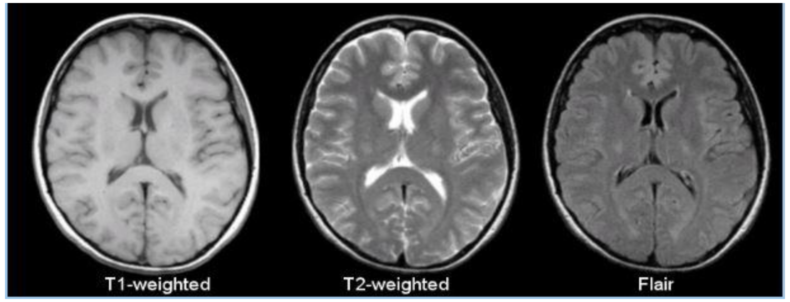


Figure 2: Different types of MRI scans; T1-weighted, T2-weighted and FLAIR [1]

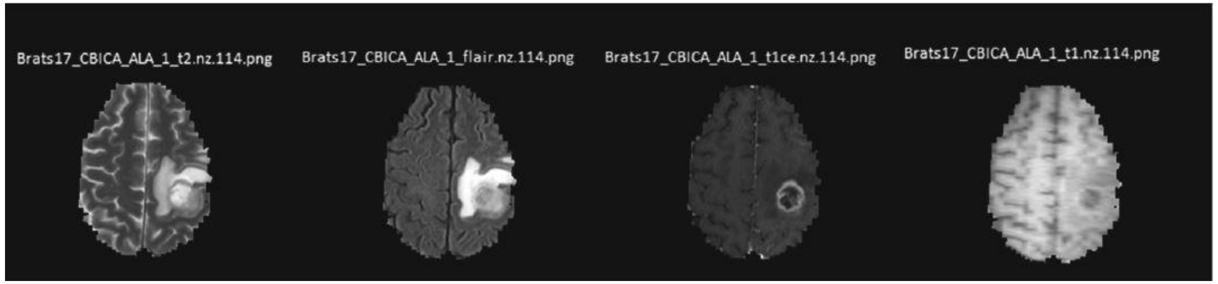


Figure 3: Four MRI scans from the same plane (top view) of a subject, a) T2-weighted, b) T2-FLAIR, c)T1-Gd, d) T1-weighted [1]

Figure 4: Ground truth labels, a) Whole Tumor, b) Core Tumor, c) Enhanced Tumor [1]

Dataset Description

Dataset Description

2

Brain Tumor Dataset
(Preprocessed BraTs 2015)

- Data obtained from The Cancer Imaging Archive
- **Dataset**: BraTs 2015 (Considered only *Low-Grade-Glioma)*
- *110 Subjects*, Each subjects consists of *40-88 images(slices)*
- **Tumor Considered:** Whole Tumor [2]
- **Preprocessed Data** :a) Skull Stripping, b) Histogram equalization (to normalize intensities)[2]

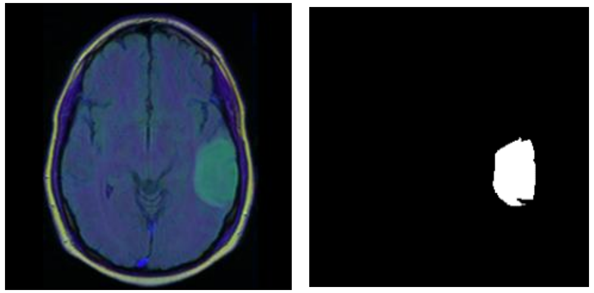


Figure 5: Sample data of brain tumor (preprocessed BraTs 2015)[2]

3

Skin Lesion Dataset

- **ISIC 2018**, which consists of a) **melanoma, b) nervus, c) seborrhoeic skin cancer [3][10]**
- Provides **2594** images with corresponding ground truth labels.

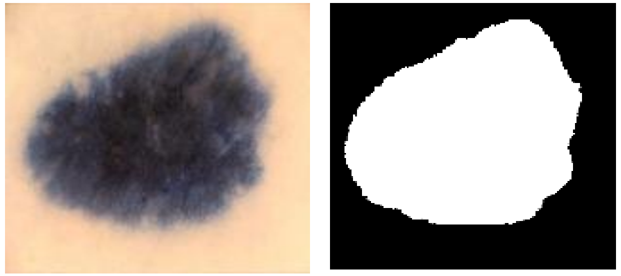


Figure 6: Sample data of Skin Cancer (ISIC 2018)[3]

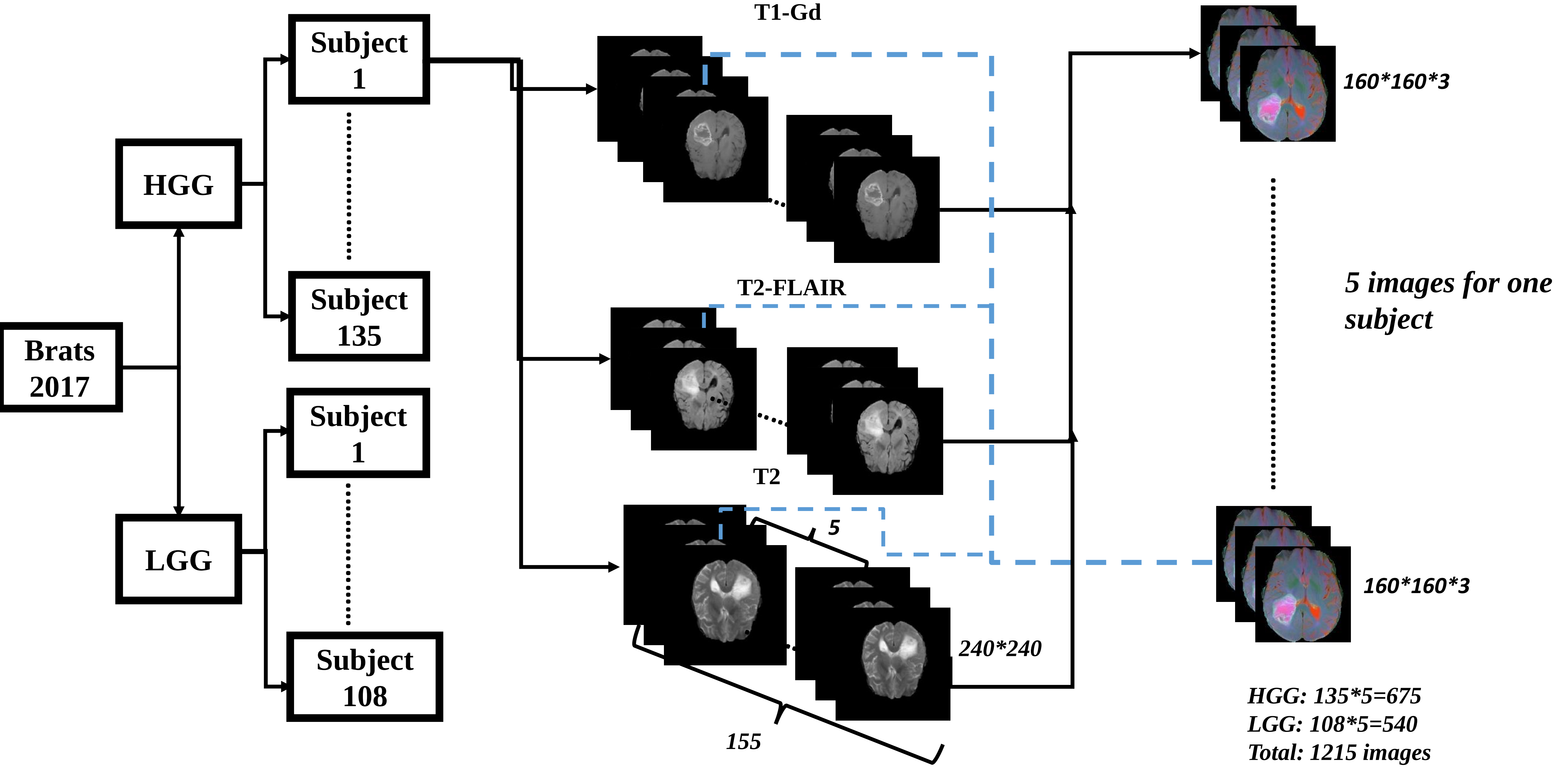
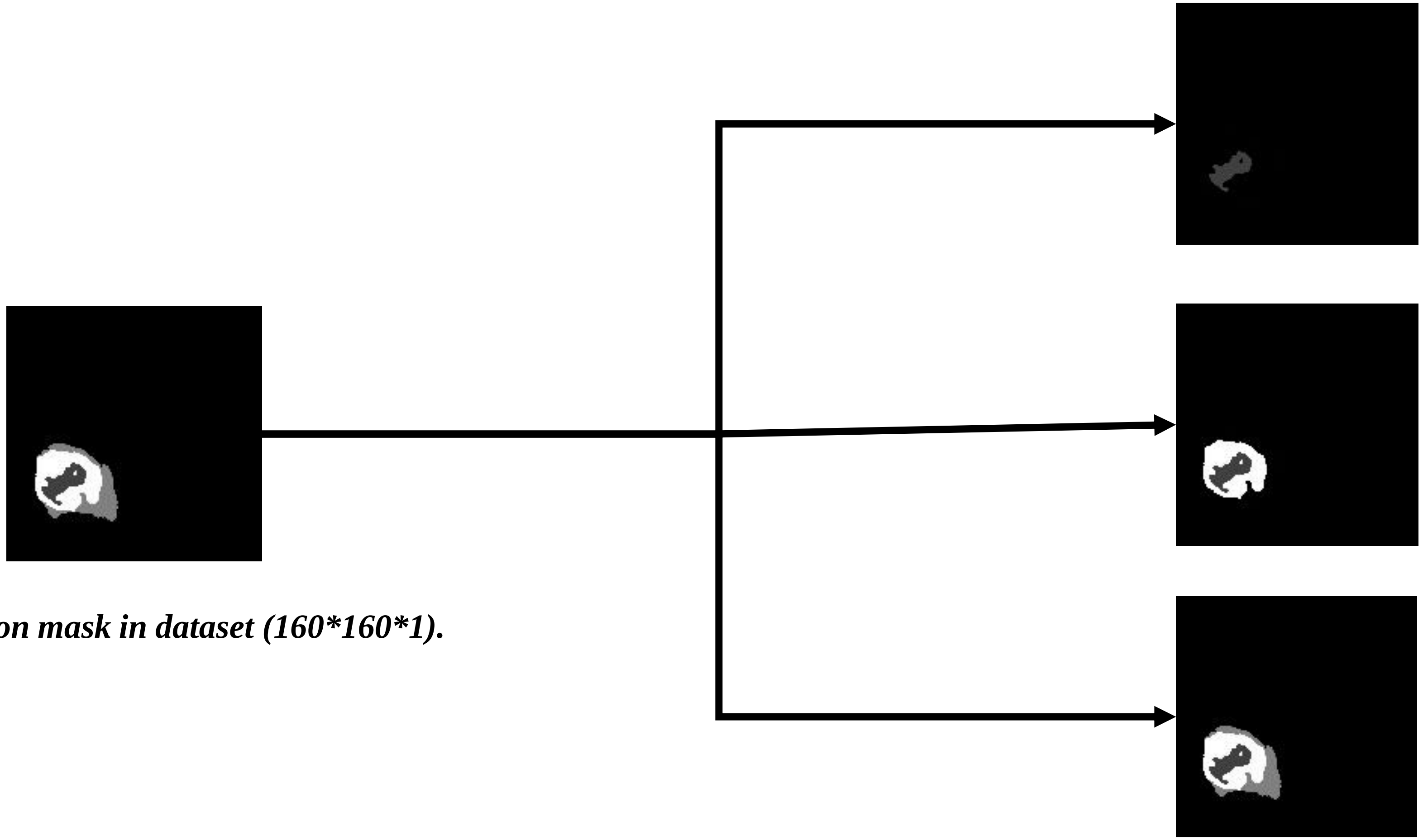


Fig 7: Flow chart for making the raw data into analysis able form.

Label Extraction



*Active Tumor 160*160*1*

*Core Tumor 160*160*1*

*Whole Tumor 160*160*1*

*Segmentation mask in dataset (160*160*1).*

Fig 8: Extracting tumors from the given mask

SegAN architecture for Bio-Medical **Image Segmentation**
BraTs 2017 brain tumor dataset

Number of Images	Data Split	Epochs	Whole		Core		Active	
			Dice	Jaccard	Dice	Jaccard	Dice	Jaccard
4000	90:10	500	0.2094	0.1599	0.2096	0.1592	0.1050	0.05
		750	0.2326	0.1746	0.2198	0.1711	0.1050	0.05
		1000	0.2450	0.1830	0.2356	0.1746	0.1152	0.06
		1500	0.2591	0.1919	0.2496	0.1836	0.1300	0.07
		2000	0.2629	0.1946	0.2512	0.1862	0.1300	0.07
		2500	**0.2656**	**0.1946**	**0.2512**	**0.1862**	**0.1350**	**0.07**

Table 1: SegAN results with BraTs 2017

Output

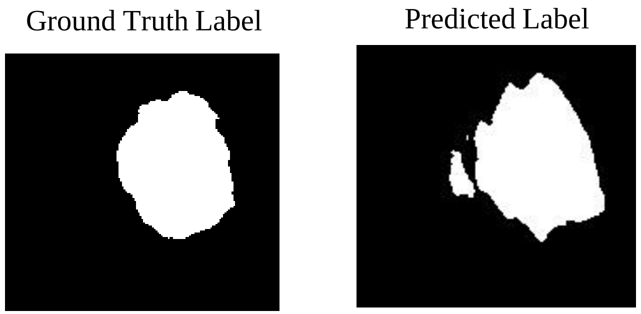


Figure 9: Segmentation output of brain tumor with SegAN (best output)

SegAN architecture for Bio-Medical **Image Segmentation** of **ISIC 2018** Skin lesion data

Results

Data Split	Epochs	Dice Score	Jaccard Index
90:10	500	68.04	56.89
	750	68.04	56.89
	1000	68.04	56.89
	1500	69.33	58.21
	2000	69.45	58.46
	2500	**69.45**	**58.46**

Table 2: SegAN results with ISIC 2018

Output

Figure 10: Segmentation output of skin tumor with SegAN

U-Net architecture for Bio-Medical **Image Segmentation** of **BraTs 2015** brain tumor processed data

Results

Data & No of Images	Data Split	Epochs	Jaccard Index	Dice Score
Without Data Augmentation 886 Images	70:30	250	70.02	83.81
	80:20	250	70.03	83.80
	90:10	250	67.75	83.80
With Data Augmentation 3544 Images	70:30	250	67.24	83.83
	80:20	250	71.26	83.84
		500	73.57	84.84
		1000	**74.23**	**85.01**
	90:10	250	68.83	83.86

Table 3: U-Net results with preprocessed BraTs 2015

Output

Ground Truth Label | Predicted Label | Ground Truth Label | Predicted Label

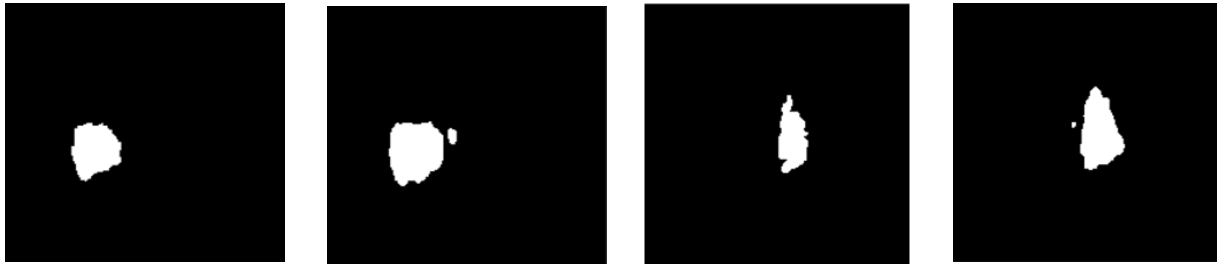


Figure 11: Segmentation output of brain tumor with U-Net

U-Net architecture for Bio-Medical **Image Segmentation** of **ISIC 2018** Skin Lesion data

Results

Data & No of Images	Data Split	Epochs	Jaccard Index	Dice Score
Without Data Augmentation 2594 Images	70:30	250	74.34	86.12
	80:20	250	75.01	86.35
	90:10	250	72.67	86.23
With Data Augmentation 10376 Images	**80:20**	250	74.32	86.43
		500	75.67	86.54
		1000	**75.96**	**87.56**

Table 4: U-Net results with ISIC 2018

Output

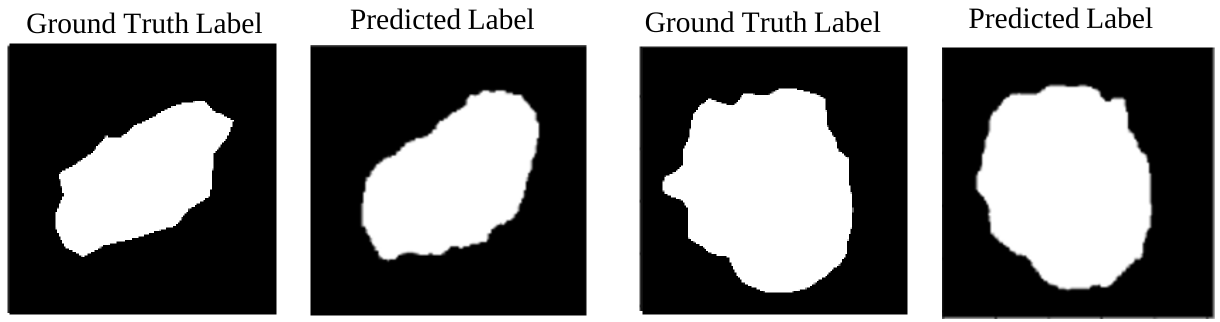


Figure 12: Segmentation output of skin lesion with U-Net

SegNet architecture for Bio-Medical **Image Segmentation** of **BraTS 2015** brain tumor processed data

Results

Data & No of Images	Data Split	Epochs	Jaccard Index	Dice Score
Without Data Augmentation 886 Images	70:30	250	66.70	81.01
	80:20	250	70.09	82.00
	90:10	250	67.74	80.01
With Data Augmentation 3544 Images	**80:20**	250	69.77	83.96
		500	71.01	83.96
		1000	**71.23**	**84.06**

Table 5: SegNet results with preprocessed BraTs 2015

Output

Ground Truth Label | Predicted Label | Ground Truth Label | Predicted Label

Figure 13: Segmentation output of brain tumor with SegNet

SegNet architecture for Bio-Medical **Image Segmentation** of **ISIC 2018** Skin lesion data

Results

Data & No of Images	Data Split	Epochs	Jaccard Index	Dice Score
Without Data Augmentation 2594 Images	70:30	250	70.30	84.67
	80:20	250	71.01	83.21
	90:10	250	66.24	81.32
With Data Augmentation 10376 Images	70:30	250	72.56	84.88
		500	72.97	85.88
		1000	**73.01**	**85.98**

Table 6: SegNet results with ISIC 2018

Output

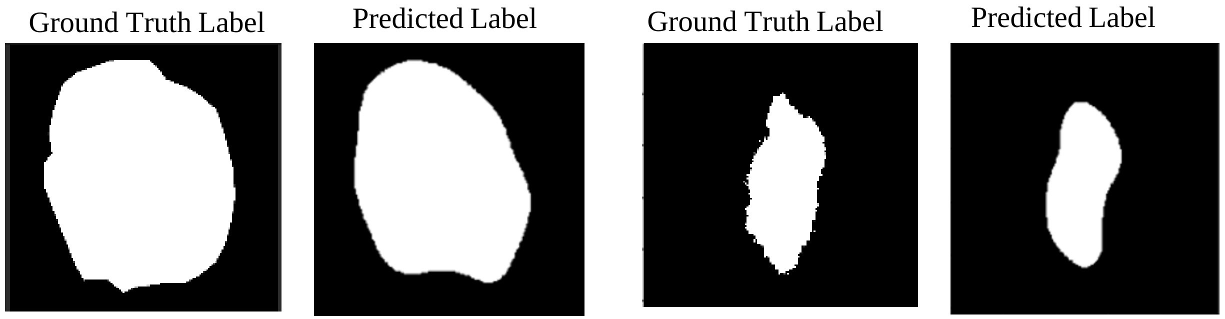


Figure 14: Segmentation output of skin lesion with SegNet

Comparison Study of **segmentation accuracy** with existing approaches

Architecture	Data Split	Epochs	Jaccard Index	Dice Score
SegAN	90:10	1000	56.89	68.04
SegNet	80:30	1000	73.01	85.98
U-Net	80:20	1000	75.96	87.56

Table 7: Results achieved by three architectures with ISIC 2018

Architecture (with ISIC 2018)	Jaccard Index	Dice Score
TernausNet [4]	82.1	-
DeepLabV3+ [4]	87.6	-
C-Unet [5]	77.5	86.5
SegAN	**56.8**	**68.04**
SegNet	**73.01**	**85.98**
U-Net	**75.96**	**87.56**

Table 9: Comparison of the proposed work with existing approaches (ISIC 2018)

Architecture	Data Split	Epochs	Jaccard Index	Dice Score
SegNet	70:30	1000	71.23	84.06
U-Net	80:20	1000	74.23	85.01

Table 8: Results achieved by two architectures with preprocessed BraTs 2015

Architecture (with Preprocessed BraTs 2015)	Jaccard Index	Dice Score
U-Net [2]	-	82
SegNet	**71.23**	**84.06**
U-Net	**74.23**	**85.01**

Table 10: Comparison of the proposed work with existing approaches (preprocessed BraTs 2015)

Comparison of **segmentation outputs** and **learnable parameters**

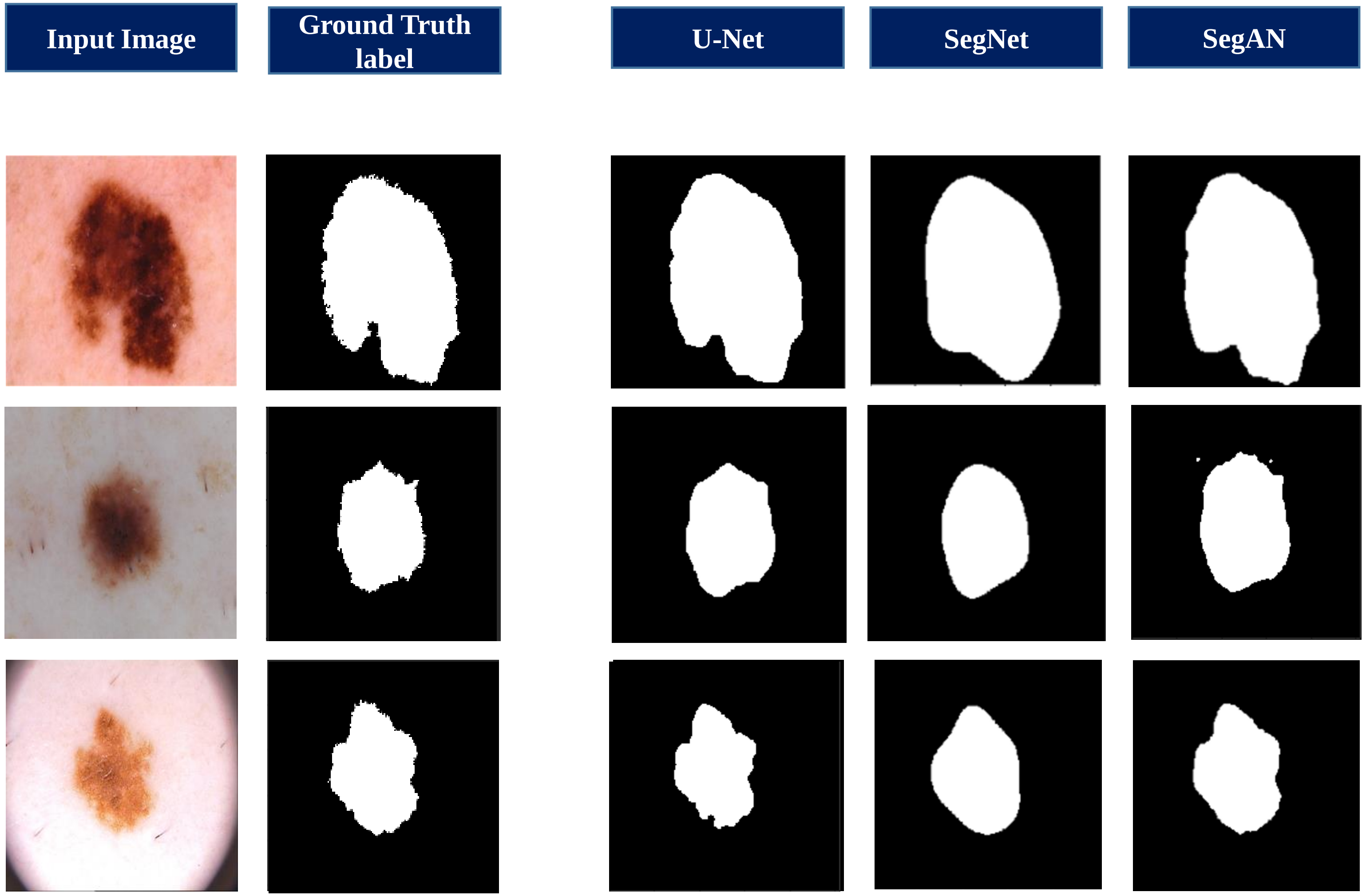


Figure 15: Comparison of segmentation output for all three architectures with ISIC 2018

Architecture	Number of Learnable Parameters	Computation time (per epochs)
SegAN [2]	222,328,178,100 (222 billion) (approx.)	1,200sec (approx.)
SegNet [6]	33,393,669 (33 million)	41 sec
U-Net [7]	31,454,721 (31 million)	30 sec

Table 11: Comparison of learnable parameter for all three architectures

Conclusion

- For Skin lesion segmentation (ISIC 2018): **U-Net > SegNet > SegAN** (in terms of Jaccard Index and Dice Score)
- For Brain tumor segmentation (Preprocessed BraTs 2015) : **U-Net > SegNet** (in terms of Jaccard Index and Dice Score)
- When compared with state of the results for **ISIC 2018 dataset**, our proposed work was able to achieve comparable results in terms of **jaccard index** and in terms of **dice score** U-Net outperformed them.
- When compared with state of the results for **preprocessed BraTs 2015,** our **U-Net** (with addition of 2 convolutional layers at encoder & decoder) and **SegNet** both outperformed the existing approach.
- Number of Learnable parameters and computation time: **SegAN > SegNet > U-Net**
- In terms of segmentation output, **U-Net** gave the sharpest edge output (which is suitable for bio-medical image segmentation), where as **SegNet** output was smooth edged.

Future Work

- Segmentation accuracy can be increased by doing more preprocessing techniques such as **haarcascade, histogram equalization .**
- The architectures such as **U-Net, C-UNet, DeepLabV3+, MobileNetV2, NasNet** is expected to increase the accuracy.

Paper (Presented)

- Sachin Saj, Sowmya V, Soman K P, **“Performance Analysis of Segmentor Adversarial Network (SegAN) on Bio-Medical Images for Image Segmentation”,** The International Conference on Automation, Signal Processing, Instrumentation and Control (i'CASIC 2020), Springer Proceeding, 27 Feb 2020 ***(Presented)***

Book Chapter (Submitted)

- Sachin Saj, Sowmya V, Soman K P, “**Performance Analysis of Deep Learning Models for Biomedical Image Segmentation**”, Book on Deep Learning for Biomedical Application, CRC Press, 2020 ***(Book Chapter Submitted)***

Reference

- Rezaei M., Harmuth K., Gierke W., Kellermeier T., Fischer M., Yang H., Meinel C, " **A Conditional Adversarial Network for Semantic Segmentation of Brain Tumor"**, International MICCAI Brainlesion Workshop, Springer. pp. 241–252, 2018.
- Yuan Xue, Tao Xu and Xiaolei Huang, **"Adversarial Learning with Multi-scale Loss for Skin Lesion segmentation"**, 15th International Symposium on Biomedical Imaging , IEEE, April 2018.
- Mateusz Buda, Ashirbani Saha, **"Association of genomic subtypes of lower-grade gliomas with shape features automatically extracted by a deep learning algorithm"**, Computers in Biology and Medicine, Elsever,. 2019.
- Jane Lameski, Andrej Jovanov, Eftim Zdravevski,**"Skin Lesion segmentation with deep learning"**, EUROCON 2019 -18th International Conference on Smart Technologies IEEE,2019
- Junyan Wu, Eric Z.Chen,"**Skin Lesion Segmentation with C-UNet**", 41st Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC)IEEE, 2019

Reference

- Jing Tang, Jun Li, “ Segnet-Based Gland Segmentation from Colon Cancer Histology Images”, The 33rd Youth Academic Annual Conference of Chinese Association of Automation, IEEE, 2018
- Olaf Ronneberger, Philpp Fischer, “U-Net Convolution Networks for Biomedical Image Segmentation”, International Conference on Medical Image Computing and Computer-Assisted Intervention, Springer, 2015.
- Bjoern H Menze, Andras Jakab, Stefan Bauer, Jayashree Kalpathy-Cramer, et al. “The Multimodal Brain Tumor Image Segmentation Benchmark (brats)”, IEEE transactions on medical imaging, IEEE transactions, 2014
- S Bakas, H Akbari, A Sotiras, M Bilello, M Rozyeki, JS Kirby, “ Advancing the cancer genome atlas glioma MRI collection with expert segmentation labels and randomic features, Scientific data, Nature, 2017
- Noel Codella, Veronica Rotemberg, Philipp Tschandil, M Emre Celebi, Stephen Susza, David Gutman, Brian Helba, et. Al, “ Skin Lesion Analysis towards Melonama detection 2018: A Challenge hosted by the international skin imaging collaboration (isic). arXiv preprint arXiv:1902.03368, 2019

Thank You

Backup Slides

Evaluation Metrics

- The most commonly used evaluation parameters for image segmentation task is :**a) Dice Score, and b) Jaccard Index**
- Both of this parameters are used in finding the similarity/overlap between the image samples: **a) Predicted image sample by the architecture, and b) ground truth image (ranges from 0-1)**

$$Dice = \frac{2\,|P \cap T|}{|P| + |T|} = \frac{2\,|P.T|}{|P|^2 + |T|^2} \qquad \textbf{Eq. (1)}$$

$$Jaccard = \frac{|P \cap T|}{|P \cup T|} = \frac{|P \cap T|}{|P| + |T| - |P \cap T|} = \frac{|P.T|}{|P|^2 + |T|^2 + |P.T|} \qquad \textbf{Eq.(2)}$$

$$Jaccard = \frac{Dice}{2 - Dice} \qquad \textbf{Eq.(3)}$$

Ground truth Label (T)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Predicted Label (P)

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$|P \cdot T| = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \cdot \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \Rightarrow \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \xRightarrow{\text{sum of elements}} 9$$

$$|P|^2 = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}^2 \xRightarrow{\text{sum of elements}} 9$$

$$|T|^2 = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}^2 \xRightarrow{\text{sum of elements}} 11$$

$$\boxed{\text{Dice} = \frac{2|P \cdot T|}{|P|^2 + |T|^2}} = \frac{2 \times 9}{9 + 11} = 0.9$$

$$\boxed{\text{Jaccard} = \frac{|P \cdot T|}{|P|^2 + |T|^2 + |P \cdot T|}} = \frac{9}{9 + 11 - 9} = 0.81$$

$$\boxed{J = \frac{D}{2 - D}} = \frac{0.9}{2 - 0.9} = 0.81$$

Architecture

Segmentor Adversarial Network (SegAN)

- **SegAN architecture** consists of two parts: **Segmentor and Critic**.
- Segmentor is an encoder-decoder network. Which is used to **generate label map** corresponding to the input.
- The **Critic** is used to **distinguish between types of inputs:** original image masked by ground truth label and original image masked by predicted label from segmentor. [2]
- The training of **Segmentor** aims at **minimizing** the multi-scale loss function and training of **Critic** aims at **maximizing** the multi-scale loss function. [2]

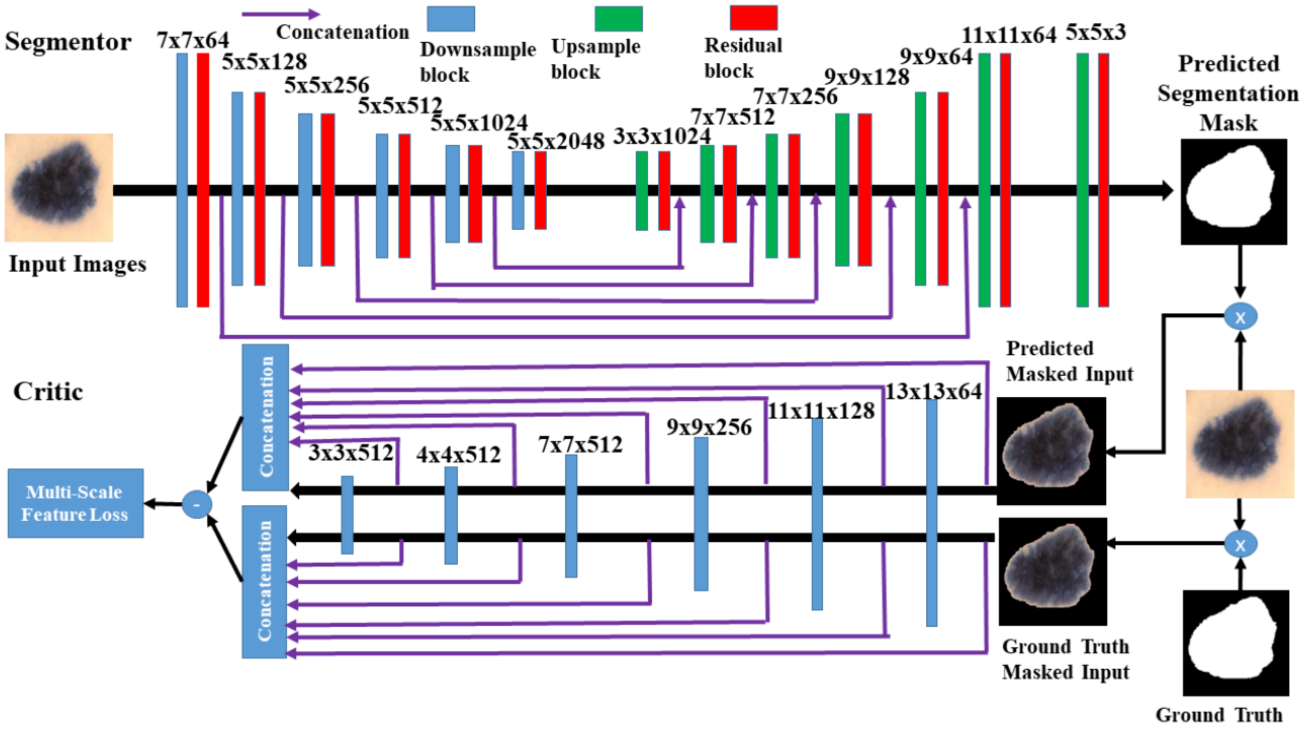


Figure 1:SegAN Architecture [2]

Architecture

U-Net Architecture

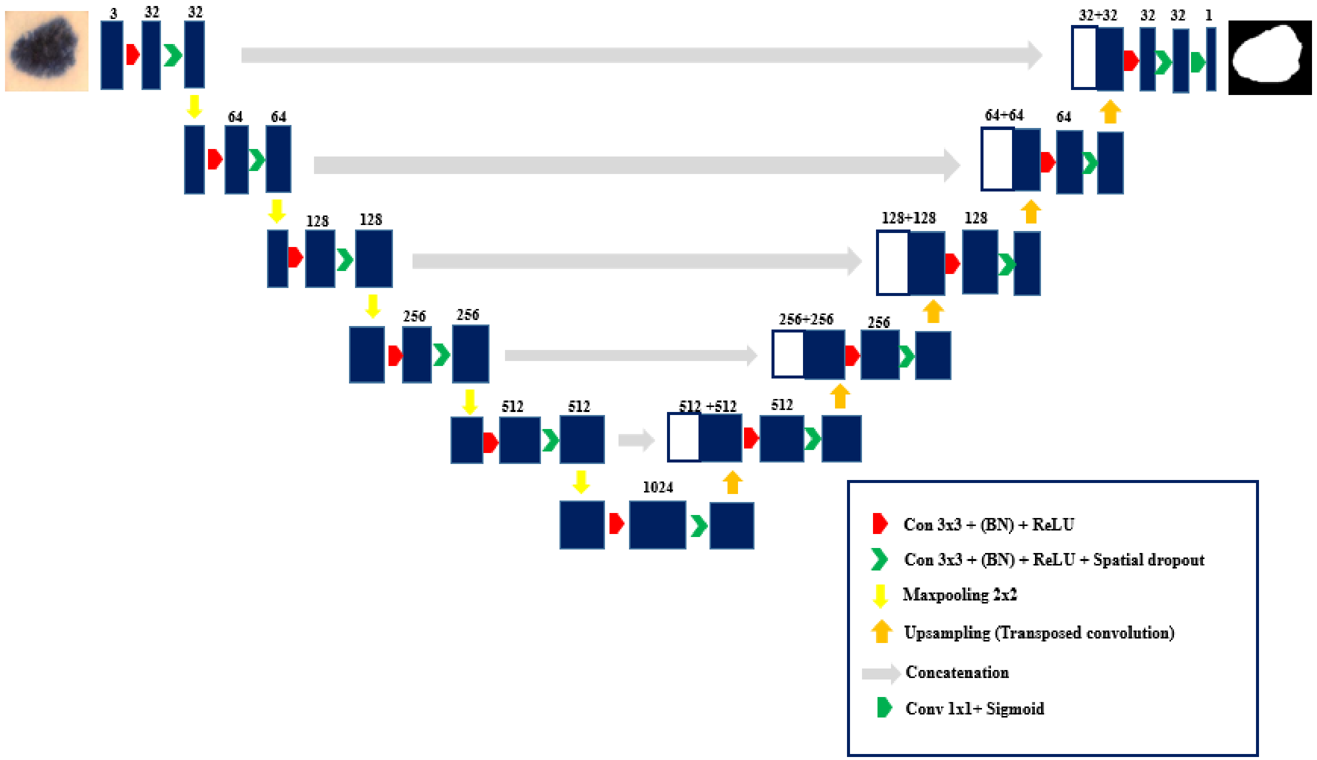


Figure 2: U-Net Architecture [7]

- U-Net is **an encoder-decoder** network
- The architecture contains **two paths**. First path is the **contraction path** (also called as the encoder) which is used to capture the context in the image. It is stack of convolutional and maxpooling layers.
- The second path is called as decoder which is more or less **symmetric expanding path** (that's why the architecture is U-shaped. which is used to enable precise localization using transposed convolutions .[7]

Architecture
SegNet Architecture

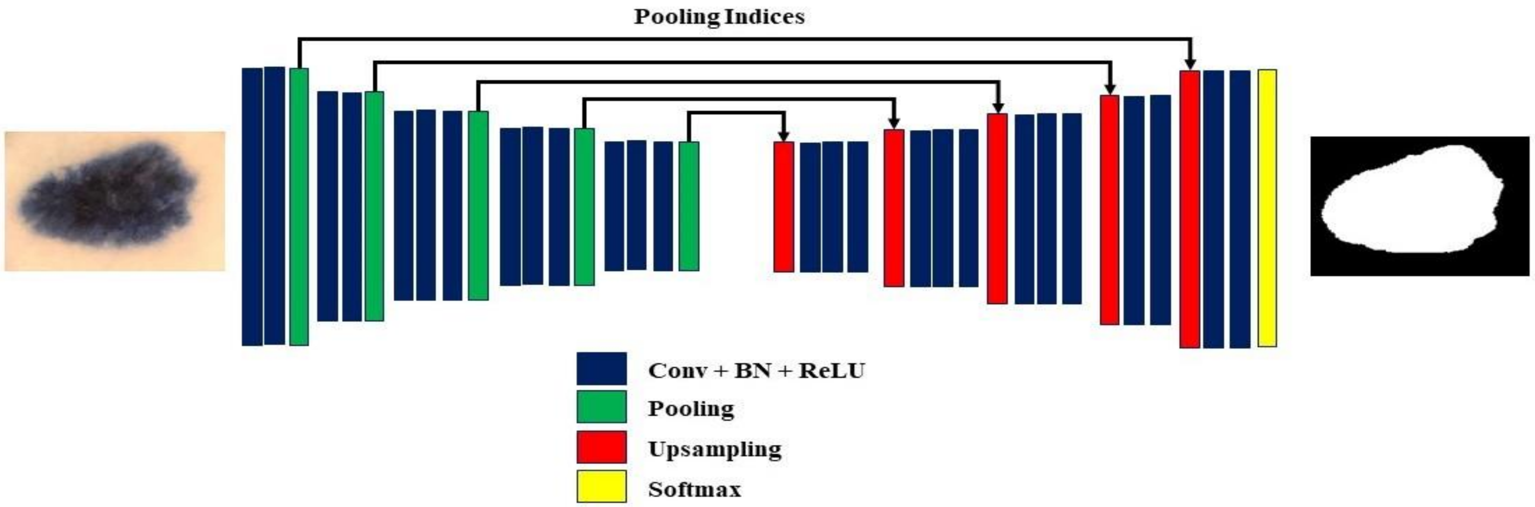


Figure 3: SegNet Architecture [6]

- SegNet is an **encoder-decoder network**
- There are **13 convolution layers** in **encoding** network as well in **decoding** network.
- Each colored box denotes different operations such as a) **blue box: Conv+BN+ReLU,** b) **green box: MaxPooling,** c**) red box: Up sampling**, and d) **yellow box: pixel-wise softmax layer**.
- Maxpooling indices is transferred from **encoder network** to **up sampling layer** of **decoder network**

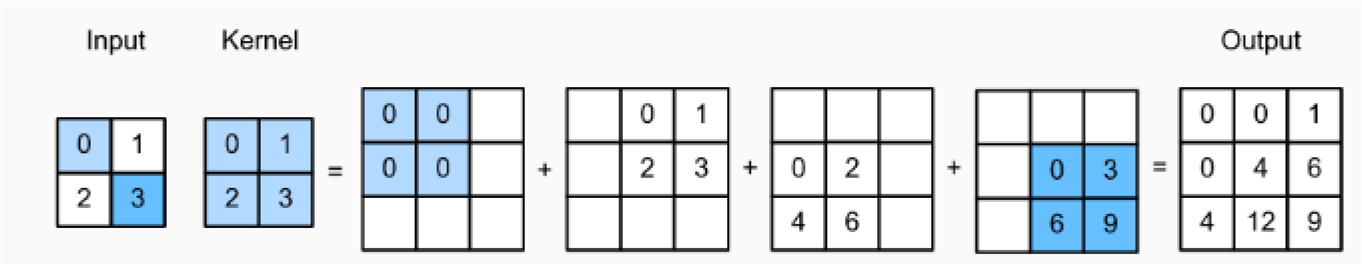


Figure 12. The Complete Transposed Convolution Operation

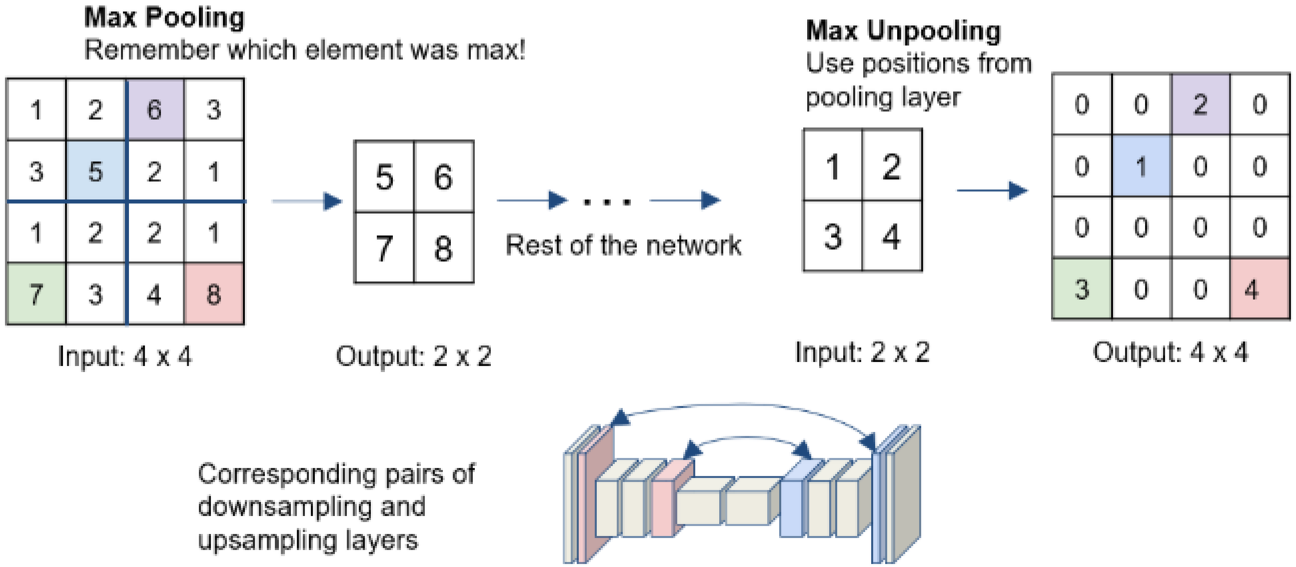


Figure 6. Max-Unpooling Upsampling